

Raw Sequence Listing

06/04/93
11:04:55
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Patent Application US/07/864,692B

15
m.B.
09/01/93

Aw 18/2

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: Israel, David
Wolfman, Neil M

(ii) TITLE OF INVENTION: RECOMBINANT BONE MORPHOGENETIC PROTEIN
HETERODIMERS, COMPOSITIONS AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140-2387

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/864,692
(B) FILING DATE: 07-APR-1992
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI-5192A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617 876-1170
(B) TELEFAX: 617 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

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53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 356..1543
57
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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61 GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT 60
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63 AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT 120
64
65 CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCCAGC 180
66
67 GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG 240
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69 GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA 300
70
71 ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG 358
72 Met
73 1
74
75 GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC 406
76 Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
77 5 10 15
78
79 CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC 454
80 Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
81 20 25 30
82
83 GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC 502
84 Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
85 35 40 45
86
87 CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG 550
88 Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
89 50 55 60 65
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91 AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC 598
92 Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
93 70 75 80
94
95 CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC 646
96 Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His
97 85 90 95
98
99 CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC 694
100 Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His
101 100 105 110
102
103 CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC 742
104 His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr

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105	115	120	125	
106				
107	CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC			790
108	Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile			
109	130	135	140	145
110				
111	ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA			838
112	Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu			
113	150	155	160	
114				
115	GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA			886
116	Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile			
117	165	170	175	
118				
119	AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC			934
120	Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp			
121	180	185	190	
122				
123	ACC AGG TTG GTG AAT CAG AAT GCA AGC AGG TGG GAA ACT TTT GAT GTC			982
124	Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp Val			
125	195	200	205	
126				
127	ACC CCC GCT GTG ATG CGG TGG ACT GCA CAG GGA CAC GCC AAC CAT GGA			1030
128	Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His Gly			
129	210	215	220	225
130				
131	TTC GTG GTG GAA GTG GCC CAC TTG GAG GAG AAA CAA GGT GTC TCC AAG			1078
132	Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser Lys			
133	230	235	240	
134				
135	AGA CAT GTT AGG ATA AGC AGG TCT TTG CAC CAA GAT GAA CAC AGC TGG			1126
136	Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser Trp			
137	245	250	255	
138				
139	TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC CAT GAT GGA AAA GGG			1174
140	Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys Gly			
141	260	265	270	
142				
143	CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC AAA CAG CGG			1222
144	His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg			
145	275	280	285	
146				
147	AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC			1270
148	Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe			
149	290	295	300	305
150				
151	AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC			1318
152	Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His			
153	310	315	320	
154				
155	GCC TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG			1366
156	Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu			

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157          325          330          335
158
159 AAC TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC      1414
160 Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn
161          340          345          350
162
163 TCT AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC      1462
164 Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile
165          355          360          365
166
167 TCG ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT      1510
168 Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr
169 370          375          380          385
170
171 CAG GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA      1563
172 Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
173          390          395
174
175 CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA      1607
176
177
178 (2) INFORMATION FOR SEQ ID NO:2:
179
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 396 amino acids
182 (B) TYPE: amino acid
183 (D) TOPOLOGY: linear
184
185 (ii) MOLECULE TYPE: protein
186
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
188
189 Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
190 1 5 10 15
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192 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
193 20 25 30
194
195 Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
196 35 40 45
197
198 Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
199 50 55 60
200
201 Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
202 65 70 75 80
203
204 Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
205 85 90 95
206
207 His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
208 100 105 110

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209
210 His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
211 115 120 125
212
213 Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
214 130 135 140
215
216 Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
217 145 150 155 160
218
219 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
220 165 170 175
221
222 Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
223 180 185 190
224
225 Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp
226 195 200 205
227
228 Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
229 210 215 220
230
231 Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
232 225 230 235 240
233
234 Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
235 245 250 255
236
237 Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
238 260 265 270
239
240 Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
241 275 280 285
242
243 Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
244 290 295 300
245
246 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
247 305 310 315 320
248
249 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
250 325 330 335
251
252 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
253 340 345 350
254
255 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
256 355 360 365
257
258 Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
259 370 375 380
260

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261 Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
262 385 390 395

263

264 (2) INFORMATION FOR SEQ ID NO:3:

265

266 (i) SEQUENCE CHARACTERISTICS:

267 (A) LENGTH: 1954 base pairs

268 (B) TYPE: nucleic acid

269 (C) STRANDEDNESS: double

270 (D) TOPOLOGY: unknown

271

272 (ii) MOLECULE TYPE: DNA

273

274

275 (ix) FEATURE:

276 (A) NAME/KEY: CDS

277 (B) LOCATION: 403..1626

278

279

280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

281

282 CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA 60

283

284 GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG 120

285

286 AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC 180

287

288 ACAGTCCCCG GCCCTCGCCC AGGTTCACCTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG 240

289

290 CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC 300

291

292 GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA 360

293

294 TCATGGACTG TTATTATATG CTTTGTTCCTG TGTCAAGACA CC ATG ATT CCT GGT 414

295

296

297

298 AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC 462

299

300

301

302 GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC 510

303

304

305

306 GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG 558

307

308

309

310 CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC 606

311

312

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314 CGC CGC CCG CAG CCT AGC AAG AGT GCC GTC ATT CCG GAC TAC ATG CGG      654
315 Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg
316      70                      75                      80
317
318 GAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAA GAG CAG ATC CAC      702
319 Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu Glu Gln Ile His
320      85                      90                      95                      100
321
322 AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC AGC CGG GCC AAC ACC      750
323 Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser Arg Ala Asn Thr
324                      105                      110                      115
325
326 GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC CCA GGG ACC      798
327 Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile Pro Gly Thr
328                      120                      125                      130
329
330 AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT      846
331 Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile Pro
332                      135                      140                      145
333
334 GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG      894
335 Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln
336                      150                      155                      160
337
338 GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT      942
339 Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile
340      165                      170                      175                      180
341
342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC      990
343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile
344                      185                      190                      195
345
346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG      1038
347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp
348                      200                      205                      210
349
350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG      1086
351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys
352                      215                      220                      225
353
354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT      1134
355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr
356                      230                      235                      240
357
358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA      1182
359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln
360      245                      250                      255                      260
361
362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC      1230
363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly
364                      265                      270                      275

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366 CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT      1278
367 His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg
368           280                      285                      290
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370 AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC      1326
371 Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys
372           295                      300                      305
373
374 CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC      1374
375 Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp
376           310                      315                      320
377
378 TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC      1422
379 Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp
380           325                      330                      335                      340
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382 TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT      1470
383 Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
384           345                      350                      355
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386 GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT      1518
387 Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys
388           360                      365                      370
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390 TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG      1566
391 Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu
392           375                      380                      385
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394 TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA      1614
395 Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly
396           390                      395                      400
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398 TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC      1666
399 Cys Gly Cys Arg
400 405
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402 CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC      1726
403
404 ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA      1786
405
406 ATCCCTAAAC ATTACCTTG ACCTTATTTA TGA CTTTACG TGCAAATGTT TTGACCATAT      1846
407
408 TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG      1906
409
410 AGTCATTATT TTAATAAAAA AAAAAAACT CTAGAGTCGA CGGAATTC      1954
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412
413 (2) INFORMATION FOR SEQ ID NO:4:
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415 (1) SEQUENCE CHARACTERISTICS:
416 (A) LENGTH: 408 amino acids
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417 (B) TYPE: amino acid
418 (D) TOPOLOGY: linear
419
420 (ii) MOLECULE TYPE: protein
421
422 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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424 Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
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427 Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
428 20 25 30
429
430 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
431 35 40 45
432
433 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
434 50 55 60
435
436 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
437 65 70 75 80
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439 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
440 85 90 95
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442 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
443 100 105 110
444
445 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
446 115 120 125
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448 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
449 130 135 140
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451 Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu
452 145 150 155 160
453
454 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
455 165 170 175
456
457 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
458 180 185 190
459
460 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
461 195 200 205
462
463 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
464 210 215 220
465
466 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
467 225 230 235 240
468

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469 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
470 245 250 255
471
472 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
473 260 265 270
474
475 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
476 275 280 285
477
478 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
479 290 295 300
480
481 Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
482 305 310 315 320
483
484 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
485 325 330 335
486
487 Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
488 340 345 350
489
490 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
491 355 360 365
492
493 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
494 370 375 380
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496 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
497 385 390 395 400
498
499 Val Val Glu Gly Cys Gly Cys Arg
500 405
501
502 (2) INFORMATION FOR SEQ ID NO:5:
503
504 (i) SEQUENCE CHARACTERISTICS:
505 (A) LENGTH: 1448 base pairs
506 (B) TYPE: nucleic acid
507 (C) STRANDEDNESS: double
508 (D) TOPOLOGY: unknown
509
510 (ii) MOLECULE TYPE: DNA
511
512
513 (ix) FEATURE:
514 (A) NAME/KEY: CDS
515 (B) LOCATION: 97..1389
516
517
518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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520 GTGACCGAGC GGC GCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG TGC GGGCCCCG

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521
522 GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGCGCG ATG CAC GTG CGC TCA CTG      114
523                               Met His Val Arg Ser Leu
524                               1                               5
525
526 CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA CCC CTG TTC      162
527 Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro Leu Phe
528           10                               15                               20
529
530 CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC GAG GTG CAC      210
531 Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu Val His
532           25                               30                               35
533
534 TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG GAG ATG      258
535 Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met
536           40                               45                               50
537
538 CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC CCG CGC CCG      306
539 Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro
540           55                               60                               65                               70
541
542 CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG      354
543 His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu
544           75                               80                               85
545
546 TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC      402
547 Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly
548           90                               95                               100
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550 TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG      450
551 Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu
552           105                               110                               115
553
554 GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG      498
555 Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met
556           120                               125                               130
557
558 AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC      546
559 Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg
560           135                               140                               145                               150
561
562 TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC CCA GAA GGG      594
563 Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly
564           155                               160                               165
565
566 GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC TAC ATC CGG      642
567 Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile Arg
568           170                               175                               180
569
570 GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG GTG CTC      690
571 Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln Val Leu
572           185                               190                               195

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573
574 CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC GAC AGC CGT      738
575 Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser Arg
576      200                      205                      210
577
578 ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC ATC ACA GCC      786
579 Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr Ala
580 215                      220                      225                      230
581
582 ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG GGC CTG CAG      834
583 Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu Gln
584      235                      240                      245
585
586 CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG GCG      882
587 Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu Ala
588      250                      255                      260
589
590 GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC TTC ATG GTG      930
591 Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met Val
592      265                      270                      275
593
594 GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC CGG TCC ACG      978
595 Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile Arg Ser Thr
596      280                      285                      290
597
598 GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC AAG AAC CAG      1026
599 Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn Gln
600 295                      300                      305                      310
601
602 GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC AGC GAC CAG      1074
603 Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln
604      315                      320                      325
605
606 AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG      1122
607 Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu
608      330                      335                      340
609
610 GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC      1170
611 Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr
612      345                      350                      355
613
614 TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC      1218
615 Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr
616      360                      365                      370
617
618 AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG      1266
619 Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr
620 375                      380                      385                      390
621
622 GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC      1314
623 Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val
624      395                      400                      405

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625
626 CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA AAC      1362
627 Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn
628          410                      415                      420
629
630 ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG      1409
631 Met Val Val Arg Ala Cys Gly Cys His
632          425                      430
633
634 ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC      1448
635
636
637 (2) INFORMATION FOR SEQ ID NO:6:
638
639     (i) SEQUENCE CHARACTERISTICS:
640         (A) LENGTH: 431 amino acids
641         (B) TYPE: amino acid
642         (D) TOPOLOGY: linear
643
644     (ii) MOLECULE TYPE: protein
645
646     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
647
648 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
649   1          5          10          15
650
651 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
652          20          25          30
653
654 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
655          35          40          45
656
657 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
658   50          55          60
659
660 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
661   65          70          75          80
662
663 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
664          85          90          95
665
666 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
667          100         105         110
668
669 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
670          115         120         125
671
672 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
673          130         135         140
674
675 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
676          145         150         155         160

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677
678 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
679 165 170 175
680
681 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
682 180 185 190
683
684 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
685 195 200 205
686
687 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
688 210 215 220
689
690 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
691 225 230 235 240
692
693 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
694 245 250 255
695
696 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
697 260 265 270
698
699 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
700 275 280 285
701
702 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
703 290 295 300
704
705 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
706 305 310 315 320
707
708 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
709 325 330 335
710
711 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
712 340 345 350
713
714 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
715 355 360 365
716
717 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
718 370 375 380
719
720 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
721 385 390 395 400
722
723 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
724 405 410 415
725
726 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
727 420 425 430
728

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729 (2) INFORMATION FOR SEQ ID NO:7:

730

731 (i) SEQUENCE CHARACTERISTICS:

732 (A) LENGTH: 2923 base pairs

733 (B) TYPE: nucleic acid

734 (C) STRANDEDNESS: double

735 (D) TOPOLOGY: circular

736

737 (ii) MOLECULE TYPE: cDNA to mRNA

738

739 (iii) HYPOTHETICAL: NO

740

741 (vi) ORIGINAL SOURCE:

742 (A) ORGANISM: Homo sapiens

743 (F) TISSUE TYPE: Human placenta

744

745 (vii) IMMEDIATE SOURCE:

746 (A) LIBRARY: Stratagene catalog #936203 Human placenta
747 cDNA library

748 (B) CLONE: BMP6C35

749

750 (viii) POSITION IN GENOME:

751 (C) UNITS: bp

752

753 (ix) FEATURE:

754 (A) NAME/KEY: CDS

755 (B) LOCATION: 160..1701

756

757 (ix) FEATURE:

758 (A) NAME/KEY: mat_peptide

759 (B) LOCATION: 1282..1698

760

761 (ix) FEATURE:

762 (A) NAME/KEY: mRNA

763 (B) LOCATION: 1..2923

764

765

766 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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768 CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC 60

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770 GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC 120

771

772 GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG 174

773

Met Pro Gly Leu Gly

774

-374 -370

775

776 CGG AGG GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC 222

777

777 Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly Leu Leu Cys Ser Cys

778

-365

-360

-355

779

780 TGC GGG CCC CCG CCG CTG CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC 270

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781	Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala	
782	-350 -345 -340	
783		
784	GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG	318
785	Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr	
786	-335 -330 -325	
787		
788	GAG CAG CCG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG	366
789	Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg	
790	-320 -315 -310	
791		
792	CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG	414
793	Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser	
794	-305 -300 -295 -290	
795		
796	GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG	462
797	Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln	
798	-285 -280 -275	
799		
800	CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG	510
801	Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln	
802	-270 -265 -260	
803		
804	CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC	558
805	Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro	
806	-255 -250 -245	
807		
808	CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG	606
809	Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu	
810	-240 -235 -230	
811		
812	GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA	654
813	Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala	
814	-225 -220 -215 -210	
815		
816	GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC GCC GCG CAC CCG	702
817	Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro	
818	-205 -200 -195	
819		
820	CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG	750
821	Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala	
822	-190 -185 -180	
823		
824	TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC TTC CTC AAC GAC GCG GAC	798
825	Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp	
826	-175 -170 -165	
827		
828	ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC	846
829	Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser	
830	-160 -155 -150	
831		
832	CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT	894

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833	Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile	
834	-145 -140 -135 -130	
835		
836	CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC	942
837	Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
838	-125 -120 -115	
839		
840	TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT	990
841	Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr	
842	-110 -105 -100	
843		
844	CAA GTC TTA CAG GAG CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG	1038
845	Gln Val Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu	
846	-95 -90 -85	
847		
848	GAC ACC CGT GTA GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC	1086
849	Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp	
850	-80 -75 -70	
851		
852	ATC ACG GCC ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG	1134
853	Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met	
854	-65 -60 -55 -50	
855		
856	GGG CTT CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC	1182
857	Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro	
858	-45 -40 -35	
859		
860	CGA GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC	1230
861	Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro	
862	-30 -25 -20	
863		
864	TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC ACC	1278
865	Phe Met Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr	
866	-15 -10 -5	
867		
868	AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC TCT ACC	1326
869	Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr	
870	1 5 10 15	
871		
872	CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT TAC AAC AGC	1374
873	Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser	
874	20 25 30	
875		
876	AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG TAT GTG AGT TTC	1422
877	Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe	
878	35 40 45	
879		
880	CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA CCC AAG GGC TAT GCT	1470
881	Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala	
882	50 55 60	
883		
884	GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC CCA CTC AAC GCA CAC ATG	1518

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885	Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met	
886	65 70 75	
887		
888	AAT GCA ACC AAC CAC GCG ATT GTG CAG ACC TTG GTT CAC CTT ATG AAC	1566
889	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn	
890	80 85 90 95	
891		
892	CCC GAG TAT GTC CCC AAA CCG TGC TGT GCG CCA ACT AAG CTA AAT GCC	1614
893	Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala	
894	100 105 110	
895		
896	ATC TCG GTT CTT TAC TTT GAT GAC AAC TCC AAT GTC ATT CTG AAA AAA	1662
897	Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys	
898	115 120 125	
899		
900	TAC AGG AAT ATG GTT GTA AGA GCT TGT GGA TGC CAC TAACTCGAAA	1708
901	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
902	130 135 140	
903		
904	CCAGATGCTG GGGACACACA TTCTGCCTTG GATTCTCTAGA TTACATCTGC CTTAAAAAAA	1768
905		
906	CACGGAAGCA CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT	1828
907		
908	TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG TAAATGACGT	1888
909		
910	GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT GTAGCATAAG GTCTGGTAAC	1948
911		
912	TGCAGAAACA TAACCGTGAA GCTCTTCCTA CCCTCCTCCC CCAAAAACCC ACCAAAATTA	2008
913		
914	GTTTTAGCTG TAGATCAAGC TATTTGGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA	2068
915		
916	AAGGAGTTAA ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT	2128
917		
918	AGATTTTACA GAGAACAGAA ATCGGGGAAG TGGGGGGAAC GCCTCTGTTC AGTTCATTCC	2188
919		
920	CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG CTCCACGGGG CGCCCTTGTC	2248
921		
922	TCAGTCATTG CTGTTGTATG TTCGTGCTGG AGTTTTGTTG GTGTGAAAAT ACACTTATTT	2308
923		
924	CAGCCAAAAC ATACCATTTC TACACCTCAA TCCTCCATTT GCTGTACTCT TTGCTAGTAC	2368
925		
926	CAAAGTAGA CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT	2428
927		
928	GAAGGCAGTG CTCACCTCTT CTTTACCAGA ACGGTTCTTT GACCAGCACA TTAACCTCTG	2488
929		
930	GACTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT GCCTTTTTTAC TATACAGCAT	2548
931		
932	ACCACGCCAC AGGGTTAGAA CCAACGAAGA AAATAAAATG AGGGTGCCCA GCTTATAAGA	2608
933		
934	ATGGTGTTAG GGGGATGAGC ATGCTGTTTA TGAACGGAAA TCATGATTTC CCTGTAGAAA	2668
935		
936	GTGAGGCTCA GATTAAATTT TAGAATATTT TCTAAATGTC TTTTTCACAA TCATGTGACT	2728

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937
938 GGGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTTGC 2788
939
940 ACTTACAGCT TTTTTTGTAATATAAACTA TAATTTATTG TCTATTTTAT ATCTGTTTTG 2848
941
942 CTGTGGCGTT GGGGGGGGGG CCGGGCTTTT GGGGGGGGGG GTTTGTTTGG GGGGTGTCGT 2908
943
944 GGTGTGGGCG GCGCG 2923
945
946

947 (2) INFORMATION FOR SEQ ID NO:8:

948 (i) SEQUENCE CHARACTERISTICS:

950 (A) LENGTH: 513 amino acids
951 (B) TYPE: amino acid
952 (D) TOPOLOGY: linear
953

954 (ii) MOLECULE TYPE: protein

955 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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957
958 Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
959 -374 -370 -365 -360
960
961 Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
962 -355 -350 -345
963
964 Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
965 -340 -335 -330
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967 Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
968 -325 -320 -315
969
970 Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
971 -310 -305 -300 -295
972
973 Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
974 -290 -285 -280
975
976 His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
977 -275 -270 -265
978
979 Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
980 -260 -255 -250
981
982 Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
983 -245 -240 -235
984
985 Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
986 -230 -225 -220 -215
987
988 Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro

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989          -210          -205          -200
990
991 Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
992          -195          -190          -185
993
994 Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
995          -180          -175          -170
996
997 Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
998          -165          -160          -155
999
1000 Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
1001          -150          -145          -140          -135
1002
1003 Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe
1004          -130          -125          -120
1005
1006 Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
1007          -115          -110          -105
1008
1009 Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
1010          -100          -95          -90
1011
1012 Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
1013          -85          -80          -75
1014
1015 Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
1016          -70          -65          -60          -55
1017
1018 Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
1019          -50          -45          -40
1020
1021 Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
1022          -35          -30          -25
1023
1024 Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val
1025          -20          -15          -10
1026
1027 His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
1028          -5          1          5          10
1029
1030 Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
1031          15          20          25
1032
1033 Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
1034          30          35          40
1035
1036 Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
1037          45          50          55
1038
1039 Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
1040          60          65          70

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1041
1042 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
1043 75 80 85 90
1044
1045 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
1046 95 100 105
1047
1048 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn
1049 110 115 120
1050
1051 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys
1052 125 130 135
1053
1054 His
1055
1056
1057

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

1061 (A) LENGTH: 2153 base pairs
1062 (B) TYPE: nucleic acid
1063 (C) STRANDEDNESS: double
1064 (D) TOPOLOGY: linear
1065

1066 (iii) HYPOTHETICAL: NO
1067

(vi) ORIGINAL SOURCE:

1069 (A) ORGANISM: Homo sapiens
1070 (H) CELL LINE: U2-OS osteosarcoma
1071

(vii) IMMEDIATE SOURCE:

1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library
1074 (B) CLONE: U2-16
1075

(viii) POSITION IN GENOME:

1077 (C) UNITS: bp
1078

(ix) FEATURE:

1080 (A) NAME/KEY: CDS
1081 (B) LOCATION: 699..2063
1082

(ix) FEATURE:

1084 (A) NAME/KEY: mat_peptide
1085 (B) LOCATION: 1647..2060
1086

(ix) FEATURE:

1088 (A) NAME/KEY: mRNA
1089 (B) LOCATION: 1..2153
1090

1091
1092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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1094 CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT      60
1095
1096 GGACTTACAG GAAGGATTTT AAGTAAATTC AGGGAAACAC ATTTACTTGA ATAGTACAAC      120
1097
1098 CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC      180
1099
1100 GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC      240
1101
1102 AGGATTTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAAGT CAAAAGCAAG TGAAGATTAC      300
1103
1104 TTTGGGAACT ACAGTTTATC AGAAGATCAA CTTTGTCTAA TTCAAATACC AAAGGCCTGA      360
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1106 TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC      420
1107
1108 TGCTACATCA ATGCAGCAAA AACTCTTAAC AACTGTGGAT AATTGGAAAT CTGAGTTTCA      480
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1110 GCTTTCCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA      540
1111
1112 TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT      600
1113
1114 TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT AAGAGGACAA      660
1115
1116 GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA      713
1117                               Met His Leu Thr Val
1118                               -316-315
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1120 TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA      761
1121 Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu
1122     -310                      -305                      -300
1123
1124 GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT      809
1125 Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser
1126     -295                      -290                      -285                      -280
1127
1128 TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG      857
1129 Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg
1130           -275                      -270                      -265
1131
1132 GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA      905
1133 Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser
1134           -260                      -255                      -250
1135
1136 CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG      953
1137 Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu
1138           -245                      -240                      -235
1139
1140 GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA      1001
1141 Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val
1142     -230                      -225                      -220
1143
1144 AGG GCA TCC TTG GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA      1049

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1145	Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro	
1146	-215 -210 -205 -200	
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1148	GCC TCT CCC AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT	1097
1149	Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr	
1150	-195 -190 -185	
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1152	CCT CTG ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC	1145
1153	Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn	
1154	-180 -175 -170	
1155		
1156	TTT CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA	1193
1157	Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu	
1158	-165 -160 -155	
1159		
1160	AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT CGA	1241
1161	Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe Arg	
1162	-150 -145 -140	
1163		
1164	TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA GCT GAA	1289
1165	Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala Ala Glu	
1166	-135 -130 -125 -120	
1167		
1168	TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA AAT GAA ACA	1337
1169	Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu Asn Glu Thr	
1170	-115 -110 -105	
1171		
1172	ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC ACA AAT AGG GAT	1385
1173	Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr Thr Asn Arg Asp	
1174	-100 -95 -90	
1175		
1176	GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC CAA GCT TTA GAT GTG	1433
1177	Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala Gln Ala Leu Asp Val	
1178	-85 -80 -75	
1179		
1180	GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC AGC AAT CAT TGG GTG ATT	1481
1181	Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser Asn His Trp Val Ile	
1182	-70 -65 -60	
1183		
1184	AAT CCC CAG AAT AAT TTG GGC TTA CAG CTC TGT GCA GAA ACA GGG GAT	1529
1185	Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys Ala Glu Thr Gly Asp	
1186	-55 -50 -45 -40	
1187		
1188	GGA CGC AGT ATC AAC GTA AAA TCT GCT GGT CTT GTG GGA AGA CAG GGA	1577
1189	Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu Val Gly Arg Gln Gly	
1190	-35 -30 -25	
1191		
1192	CCT CAG TCA AAA CAA CCA TTC ATG GTG GCC TTC TTC AAG GCG AGT GAG	1625
1193	Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Ser Glu	
1194	-20 -15 -10	
1195		
1196	GTA CTT CTT CGA TCC GTG AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC	1673

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1197 Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn
1198 -5 1 5
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1200 CGC AAT AAA TCC AGC TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT 1721
1201 Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser Arg Met Ser Ser Val
1202 10 15 20 25
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1204 GGA GAT TAT AAC ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA 1769
1205 Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys His Glu
1206 30 35 40
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1208 CTC TAT GTG AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA 1817
1209 Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
1210 45 50 55
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1212 CCA GAA GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA 1865
1213 Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro
1214 60 65 70
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1216 CTT AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG 1913
1217 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
1218 75 80 85
1219
1220 GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT CCA 1961
1221 Val His Leu Met Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala Pro
1222 90 95 100 105
1223
1224 ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC TCC AAT 2009
1225 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn
1226 110 115 120
1227
1228 GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA TGT GGC TGC 2057
1229 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ser Cys Gly Cys
1230 125 130 135
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1232 CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT TAAGGTTTAT 2110
1233 His
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1236 GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA 2153
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1239 (2) INFORMATION FOR SEQ ID NO:10:
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1241 (i) SEQUENCE CHARACTERISTICS:
1242 (A) LENGTH: 454 amino acids
1243 (B) TYPE: amino acid
1244 (D) TOPOLOGY: linear
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1246 (ii) MOLECULE TYPE: protein
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1248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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1253 Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn
1254 -300 -295 -290 -285
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1256 His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg
1257 -280 -275 -270
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1259 Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
1260 -265 -260 -255
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1262 Pro Arg Pro Phe Ser Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala
1263 -250 -245 -240
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1265 Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu
1266 -235 -230 -225
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1268 Ser Glu Tyr Ser Val Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala
1269 -220 -215 -210 -205
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1271 Arg Lys Gly Tyr Pro Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln
1272 -200 -195 -190
1273
1274 Leu Ser Arg Thr Thr Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser
1275 -185 -180 -175
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1277 Leu His Asp Thr Asn Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe
1278 -170 -165 -160
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1280 Val Asn Leu Val Glu Arg Asp Lys Asp Phe Ser His Gln Arg Arg His
1281 -155 -150 -145
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1283 Tyr Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala
1284 -140 -135 -130 -125
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1286 Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg
1287 -120 -115 -110
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1289 Phe Glu Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu
1290 -105 -100 -95
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1292 Tyr Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala
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1295 Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser
1296 -75 -70 -65
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1298 Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys
1299 -60 -55 -50 -45
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1301 Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu
1302 -40 -35 -30
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1304 Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe
1305 -25 -20 -15
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1307 Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys
1308 -10 -5 1
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1310 Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser
1311 5 10 15 20
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1313 Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala
1314 25 30 35
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1316 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1317 40 45 50
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1319 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
1320 55 60 65
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1322 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
1323 70 75 80
1324
1325 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
1326 85 90 95 100
1327
1328 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
1329 105 110 115
1330
1331 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
1332 120 125 130
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1334 Arg Ser Cys Gly Cys His
1335 135
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1337

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human Heart

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1353
1354 (vii) IMMEDIATE SOURCE:
1355 (A) LIBRARY: Human heart cDNA library stratagene catalog
1356 #936208
1357 (B) CLONE: hH38
1358
1359 (viii) POSITION IN GENOME:
1360 (C) UNITS: bp
1361
1362 (ix) FEATURE:
1363 (A) NAME/KEY: CDS
1364 (B) LOCATION: 8..850
1365
1366 (ix) FEATURE:
1367 (A) NAME/KEY: mat_peptide
1368 (B) LOCATION: 427..843
1369
1370 (ix) FEATURE:
1371 (A) NAME/KEY: mRNA
1372 (B) LOCATION: 1..997
1373
1374
1375 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
1376
1377 GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49
1378 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile
1379 -139 -135 -130
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1381 CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97
1382 Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val
1383 -125 -120 -115 -110
1384
1385 CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG 145
1386 Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln
1387 -105 -100 -95
1388
1389 GTG GTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 193
1390 Val Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
1391 -90 -85 -80
1392
1393 CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC 241
1394 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val
1395 -75 -70 -65
1396
1397 ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA 289
1398 Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly
1399 -60 -55 -50
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1401 CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC GTG GAT CCT GGC 337
1402 Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly
1403 -45 -40 -35 -30
1404

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1405 CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC      385
1406 Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe
1407          -25                      -20                      -15
1408
1409 GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG      433
1410 Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg
1411          -10                      -5                      1
1412
1413 GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG      481
1414 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
1415          5                      10                      15
1416
1417 CCG CAG GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC      529
1418 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser
1419    20                      25                      30                      35
1420
1421 CAC GGC CGG CAG GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG      577
1422 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
1423          40                      45                      50
1424
1425 GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC      625
1426 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
1427          55                      60                      65
1428
1429 TAT TAC TGT GAG GGG GAG TGC TCC TTC CCG CTG GAC TCC TGC ATG AAC      673
1430 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
1431          70                      75                      80
1432
1433 GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA      721
1434 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
1435          85                      90                      95
1436
1437 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC      769
1438 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
1439    100                      105                      110                      115
1440
1441 TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC      817
1442 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
1443          120                      125                      130
1444
1445 CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC      870
1446 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
1447          135                      140
1448
1449 TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC      930
1450
1451 TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG      990
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1453 CTTCTGGGAA TTC      1003
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1455
1456 (2) INFORMATION FOR SEQ ID NO:12:

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1457
1458 (i) SEQUENCE CHARACTERISTICS:
1459 (A) LENGTH: 281 amino acids
1460 (B) TYPE: amino acid
1461 (D) TOPOLOGY: linear
1462
1463 (ii) MOLECULE TYPE: protein
1464
1465 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
1466
1467 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
1468 -139 -135 -130 -125
1469
1470 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser
1471 -120 -115 -110
1472
1473 Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val
1474 -105 -100 -95
1475
1476 Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
1477 -90 -85 -80
1478
1479 Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala
1480 -75 -70 -65 -60
1481
1482 Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg
1483 -55 -50 -45
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1485 Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala
1486 -40 -35 -30
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1488 Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
1489 -25 -20 -15
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1491 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val
1492 -10 -5 1 5
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1494 Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
1495 10 15 20
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1497 Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly
1498 25 30 35
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1500 Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu
1501 40 45 50
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1503 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
1504 55 60 65
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1506 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
1507 70 75 80 85
1508

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1509 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
1510 90 95 100
1511
1512 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
1513 105 110 115
1514
1515 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
1516 120 125 130
1517
1518 Met Val Val Lys Ala Cys Gly Cys His
1519 135 140
1520

1521 (2) INFORMATION FOR SEQ ID NO:13:

1522

1523 (i) SEQUENCE CHARACTERISTICS:

1524 (A) LENGTH: 3623 base pairs

1525 (B) TYPE: nucleic acid

1526 (C) STRANDEDNESS: double

1527 (D) TOPOLOGY: linear

1528

1529 (ii) MOLECULE TYPE: DNA

1530

1531

1532 (vii) IMMEDIATE SOURCE:

1533 (B) CLONE: pALBP2-781

1534

1535 (ix) FEATURE:

1536 (A) NAME/KEY: CDS

1537 (B) LOCATION: 2724..3071

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1539 (ix) FEATURE:

1540 (A) NAME/KEY: terminator

1541 (B) LOCATION: 3150..3218

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1543 (ix) FEATURE:

1544 (A) NAME/KEY: RBS

1545 (B) LOCATION: 2222..2723

1546

1547

1548 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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1552 CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 120

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1554 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT 180

1555

1556 AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT 240

1557

1558 TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 300

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1560 CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA 360

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1561
1562 TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC 420
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1564 TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC 480
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1566 ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG 540
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1568 GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 600
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1570 ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG 660
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1572 GGGATCATGT AACTCGCCTT GATCGTTGGG AACC GGAGCT GAATGAAGCC ATACCAAACG 720
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1582 CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC 1020
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1610 GGGGGCGGAG CCTATGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT 1860
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1612 GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA 1920

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1613
1614 TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT 1980
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1616 CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC 2040
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1618 CGATTCATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCCCTT GCAAAAAATA 2100
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1620 AATTCATATA AAAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160
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1622 GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA 2220
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1624 AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG 2280
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1626 GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCCGGATTA GCTGCCAATG 2340
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1628 TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAACTGCC ACACACCACC AAAGCTAACT 2400
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1630 GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG 2460
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1632 GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA 2520
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1634 GATTTTTTTT ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC 2580
1635
1636 GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA 2640
1637
1638 GGGCATCAAA TTAACCACA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT 2700
1639
1640 GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA 2750
1641 Met Gln Ala Lys His Lys Lys Gln Arg Lys
1642 1 5
1643
1644 CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT 2798
1645 Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
1646 10 15 20 25
1647
1648 GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC 2846
1649 Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala
1650 30 35 40
1651
1652 TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC 2894
1653 Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn
1654 45 50 55
1655
1656 TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT 2942
1657 Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser
1658 60 65 70
1659
1660 AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG 2990
1661 Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser
1662 75 80 85
1663
1664 ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG 3038

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	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	
1666	90					95				100						105	
1667																	
1668	GAC	ATG	GTT	GTG	GAG	GGT	TGT	GGG	TGT	CGC	TAGTACAGCA	AAATTAAATA					3088
1669	Asp	Met	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg							
1670					110				115								
1671																	
1672	CATAAATATA	TATATATATA	TATATTTTAG	AAAAAAGAAA	AAAATCTAGA	GTCGACCTGC											3148
1673																	
1674	AGTAATCGTA	CAGGGTAGTA	CAAATAAAAA	AGGCACGTCA	GATGACGTGC	CTTTTTTCTT											3208
1675																	
1676	GTGAGCAGTA	AGCTTGGCAC	TGGCCGTCGT	TTTACAACGT	CGTGACTGGG	AAAACCCTGG											3268
1677																	
1678	CGTTACCCAA	CTTAATCGCC	TTGCAGCAC	TCCCCCTTTC	GCCAGCTGGC	GTAATAGCGA											3328
1679																	
1680	AGAGGCCCGC	ACCGATCGCC	CTTCCAACA	GTTGCGCAGC	CTGAATGGCG	AATGGCGCCT											3388
1681																	
1682	GATGCGGTAT	TTTCTCCTTA	CGCATCTGTG	CGGTATTTCA	CACCGCATAT	ATGGTGCAC											3448
1683																	
1684	CTCAGTACAA	TCTGCTCTGA	TGCCGCATAG	TTAAGCCAGC	CCCACACCC	GCCAACACCC											3508
1685																	
1686	GCTGACGCGC	CCTGACGGGC	TTGTCTGCTC	CCGGCATCCG	CTTACAGACA	AGCTGTGACC											3568
1687																	
1688	GTCTCCGGGA	GCTGCATGTG	TCAGAGGTTT	TCACCGTCAT	CACCGAAACG	CGCGA											3623
1689																	
1690																	
1691	(2)	INFORMATION FOR SEQ ID NO:14:															
1692																	
1693	(i)	SEQUENCE CHARACTERISTICS:															
1694		(A) LENGTH: 115 amino acids															
1695		(B) TYPE: amino acid															
1696		(D) TOPOLOGY: linear															
1697																	
1698	(ii)	MOLECULE TYPE: protein															
1699																	
1700	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:14:															
1701																	
1702	Met	Gln	Ala	Lys	His	Lys	Gln	Arg	Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	
1703	1				5					10					15		
1704																	
1705	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	
1706				20					25					30			
1707																	

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1717 Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn
1718 85 90 95
1719
1720 Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys
1721 100 105 110
1722
1723 Gly Cys Arg
1724 115
1725
1726

1727 (2) INFORMATION FOR SEQ ID NO:15:

1728
1729 (i) SEQUENCE CHARACTERISTICS:
1730 (A) LENGTH: 14 base pairs
1731 (B) TYPE: nucleic acid
1732 (C) STRANDEDNESS: single
1733 (D) TOPOLOGY: linear
1734

1735 (ii) MOLECULE TYPE: DNA
1736
1737
1738

1739 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

1740
1741 CATGGGCAGC TGAG
1742

14

1743 (2) INFORMATION FOR SEQ ID NO:16:

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1745 (i) SEQUENCE CHARACTERISTICS:
1746 (A) LENGTH: 41 base pairs
1747 (B) TYPE: nucleic acid
1748 (C) STRANDEDNESS: single
1749 (D) TOPOLOGY: linear
1750

1751 (ii) MOLECULE TYPE: DNA
1752
1753
1754

1755 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

1756
1757 GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T
1758

41

1759 (2) INFORMATION FOR SEQ ID NO:17:

1760
1761 (i) SEQUENCE CHARACTERISTICS:
1762 (A) LENGTH: 38 base pairs
1763 (B) TYPE: nucleic acid
1764 (C) STRANDEDNESS: single
1765 (D) TOPOLOGY: linear
1766

1767 (ii) MOLECULE TYPE: DNA
1768

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1769
1770
1771 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
1772
1773 GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC 38
1774
1775 (2) INFORMATION FOR SEQ ID NO:18:
1776
1777 (i) SEQUENCE CHARACTERISTICS:
1778 (A) LENGTH: 31 base pairs
1779 (B) TYPE: nucleic acid
1780 (C) STRANDEDNESS: single
1781 (D) TOPOLOGY: linear
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1783 (ii) MOLECULE TYPE: DNA
1784
1785
1786
1787 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
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1789 AATTCACCAT GATTCCTGGT AACCGAATGC T 31
1790
1791 (2) INFORMATION FOR SEQ ID NO:19:
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1793 (i) SEQUENCE CHARACTERISTICS:
1794 (A) LENGTH: 25 base pairs
1795 (B) TYPE: nucleic acid
1796 (C) STRANDEDNESS: single
1797 (D) TOPOLOGY: linear
1798
1799 (ii) MOLECULE TYPE: DNA
1800
1801
1802
1803 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
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1805 GTGGTACTAA GGACCATTGG CTTAC 25
1806
1807 (2) INFORMATION FOR SEQ ID NO:20:
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1809 (i) SEQUENCE CHARACTERISTICS:
1810 (A) LENGTH: 27 base pairs
1811 (B) TYPE: nucleic acid
1812 (C) STRANDEDNESS: single
1813 (D) TOPOLOGY: linear
1814
1815 (ii) MOLECULE TYPE: DNA
1816
1817
1818
1819 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
1820

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1821 CGACCTGCAG CCATGCATCT GACTGTA 27
1822
1823 (2) INFORMATION FOR SEQ ID NO:21:
1824
1825 (i) SEQUENCE CHARACTERISTICS:
1826 (A) LENGTH: 27 base pairs
1827 (B) TYPE: nucleic acid
1828 (C) STRANDEDNESS: single
1829 (D) TOPOLOGY: linear
1830
1831 (ii) MOLECULE TYPE: DNA
1832
1833
1834
1835 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
1836
1837 TGCCTGCAGT TTAATATTAG TGGCAGC 27
1838
1839 (2) INFORMATION FOR SEQ ID NO:22:
1840
1841 (i) SEQUENCE CHARACTERISTICS:
1842 (A) LENGTH: 15 base pairs
1843 (B) TYPE: nucleic acid
1844 (C) STRANDEDNESS: single
1845 (D) TOPOLOGY: linear
1846
1847 (ii) MOLECULE TYPE: DNA
1848
1849
1850
1851 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
1852
1853 CGACCTGCAG CCACC 15
1854
1855 (2) INFORMATION FOR SEQ ID NO:23:
1856
1857 (i) SEQUENCE CHARACTERISTICS:
1858 (A) LENGTH: 81 base pairs
1859 (B) TYPE: nucleic acid
1860 (C) STRANDEDNESS: single
1861 (D) TOPOLOGY: linear
1862
1863 (ii) MOLECULE TYPE: DNA
1864
1865
1866
1867 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
1868
1869 TCGACCCACC ATGCCGGGGC TGGGGCGGAG GGCGCAGTGG CTGTGCTGGT GGTGGGGGGCT 60
1870
1871 GTGCTGCAGC TGCTGCGGGC C 81
1872

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1873 (2) INFORMATION FOR SEQ ID NO:24:
1874
1875 (i) SEQUENCE CHARACTERISTICS:
1876 (A) LENGTH: 73 base pairs
1877 (B) TYPE: nucleic acid
1878 (C) STRANDEDNESS: single
1879 (D) TOPOLOGY: linear
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1881 (ii) MOLECULE TYPE: DNA
1882
1883
1884
1885 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
1886
1887 CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60
1888
1889 CCGGCATGGT GGG 73
1890
1891 (2) INFORMATION FOR SEQ ID NO:25:
1892
1893 (i) SEQUENCE CHARACTERISTICS:
1894 (A) LENGTH: 11 base pairs
1895 (B) TYPE: nucleic acid
1896 (C) STRANDEDNESS: single
1897 (D) TOPOLOGY: linear
1898
1899 (ii) MOLECULE TYPE: DNA
1900
1901
1902
1903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
1904
1905 TCGACTGGTT T 11
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1907 (2) INFORMATION FOR SEQ ID NO:26:
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1909 (i) SEQUENCE CHARACTERISTICS:
1910 (A) LENGTH: 9 base pairs
1911 (B) TYPE: nucleic acid
1912 (C) STRANDEDNESS: single
1913 (D) TOPOLOGY: linear
1914
1915 (ii) MOLECULE TYPE: DNA
1916
1917
1918
1919 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
1920
1921 CGAAACCAG 9
1922
1923 (2) INFORMATION FOR SEQ ID NO:27:
1924

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1925 (i) SEQUENCE CHARACTERISTICS:
1926 (A) LENGTH: 18 base pairs
1927 (B) TYPE: nucleic acid
1928 (C) STRANDEDNESS: single
1929 (D) TOPOLOGY: linear
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1931 (ii) MOLECULE TYPE: DNA
1932
1933
1934 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
1935
1936 TCGACAGGCT CGCCTGCA 18
1937
1938 (2) INFORMATION FOR SEQ ID NO:28:
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1940 (i) SEQUENCE CHARACTERISTICS:
1941 (A) LENGTH: 10 base pairs
1942 (B) TYPE: nucleic acid
1943 (C) STRANDEDNESS: single
1944 (D) TOPOLOGY: linear
1945
1946 (ii) MOLECULE TYPE: DNA
1947
1948
1949
1950 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
1951
1952 GTCCGAGCGG 10
1953
1954 (2) INFORMATION FOR SEQ ID NO:29:
1955
1956 (i) SEQUENCE CHARACTERISTICS:
1957 (A) LENGTH: 29 base pairs
1958 (B) TYPE: nucleic acid
1959 (C) STRANDEDNESS: single
1960 (D) TOPOLOGY: linear
1961
1962 (ii) MOLECULE TYPE: DNA
1963
1964
1965
1966 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
1967
1968 CAGGTCGACC CACCATGCAC GTGCGCTCA 29
1969
1970 (2) INFORMATION FOR SEQ ID NO:30:
1971
1972 (i) SEQUENCE CHARACTERISTICS:
1973 (A) LENGTH: 27 base pairs
1974 (B) TYPE: nucleic acid
1975 (C) STRANDEDNESS: single
1976 (D) TOPOLOGY: linear

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1977
1978 (ii) MOLECULE TYPE: DNA
1979
1980
1981
1982 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1983
1984 TCTGTCGACC TCGGAGGAGC TAGTGGC 27
1985
1986 (2) INFORMATION FOR SEQ ID NO:31:
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1988 (i) SEQUENCE CHARACTERISTICS:
1989 (A) LENGTH: 1794 base pairs
1990 (B) TYPE: nucleic acid
1991 (C) STRANDEDNESS: double
1992 (D) TOPOLOGY: linear
1993
1994 (ii) MOLECULE TYPE: DNA
1995
1996 (vi) ORIGINAL SOURCE:
1997 (A) ORGANISM: bmp-3
1998
1999 (ix) FEATURE:
2000 (A) NAME/KEY: CDS
2001 (B) LOCATION: 321..1136
2002
2003
2004 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
2005
2006 AGATCTTGAA AACACCCGGG CCACACACGC CGCGACCTAC AGCTCTTTCT CAGCGTTGGA 60
2007
2008 GTGGAGACGG CGCCCGCAGC GCCCTGCGCG GGTGAGGTCC GCGCAGCTGC TGGGGAAGAG 120
2009
2010 CCCACCTGTC AGGCTGCGCT GGGTCAGCGC AGCAAGTGGG GCTGGCCGCT ATCTCGCTGC 180
2011
2012 ACCCGGCCGC GTCCCGGGCT CCGTGCGCC CCGCCCGAGC TGGTTTGGAG TTCAACCCTC 240
2013
2014 GGCTCCGCCG CCGGCTCCTT GCGCCTTCGG AGTGTCCGC AGCGACGCCG GGAGCCGACG 300
2015
2016 CGCCGCGCGG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC TTT CTG 350
2017 Met Ala Gly Ala Ser Arg Leu Leu Phe Leu
2018 1 5 10
2019
2020 TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CCG AAG 398
2021 Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys
2022 15 20 25
2023
2024 CCA CCT TTC CCG GAG CTC CGC AAA GCT GTG CCA GGT GAC CGC ACG GCA 446
2025 Pro Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala
2026 30 35 40
2027
2028 GGT GGT GGC CCG GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA 494

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2029	Gly	Gly	Gly	Pro	Asp	Ser	Glu	Leu	Gln	Pro	Gln	Asp	Lys	Val	Ser	Glu	
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2031																	
2032	CAC	ATG	CTG	CGG	CTC	TAT	GAC	AGG	TAC	AGC	ACG	GTC	CAG	GCG	GCC	CGG	542
2033	His	Met	Leu	Arg	Leu	Tyr	Asp	Arg	Tyr	Ser	Thr	Val	Gln	Ala	Ala	Arg	
2034		60					65					70					
2035																	
2036	ACA	CCG	GGC	TCC	CTG	GAG	GGA	GGC	TCG	CAG	CCC	TGG	CGC	CCT	CGG	CTC	590
2037	Thr	Pro	Gly	Ser	Leu	Glu	Gly	Gly	Ser	Gln	Pro	Trp	Arg	Pro	Arg	Leu	
2038		75				80				85						90	
2039																	
2040	CTG	CGC	GAA	GGC	AAC	ACG	GTT	CGC	AGC	TTT	CGG	GCG	GCA	GCA	GCA	GAA	638
2041	Leu	Arg	Glu	Gly	Asn	Thr	Val	Arg	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Glu	
2042					95					100					105		
2043																	
2044	ACT	CTT	GAA	AGA	AAA	GGA	CTG	TAT	ATC	TTC	AAT	CTG	ACA	TCG	CTA	ACC	686
2045	Thr	Leu	Glu	Arg	Lys	Gly	Leu	Tyr	Ile	Phe	Asn	Leu	Thr	Ser	Leu	Thr	
2046				110					115					120			
2047																	
2048	AAG	TCT	GAA	AAC	ATT	TTG	TCT	GCC	ACA	CTG	TAT	TTC	TGT	ATT	GGA	GAG	734
2049	Lys	Ser	Glu	Asn	Ile	Leu	Ser	Ala	Thr	Leu	Tyr	Phe	Cys	Ile	Gly	Glu	
2050			125					130					135				
2051																	
2052	CTA	GGA	AAC	ATC	AGC	CTG	AGT	TGT	CCA	GTG	TCT	GGA	GGA	TGC	TCC	CAT	782
2053	Leu	Gly	Asn	Ile	Ser	Leu	Ser	Cys	Pro	Val	Ser	Gly	Gly	Cys	Ser	His	
2054		140					145					150					
2055																	
2056	CAT	GCT	CAG	AGG	AAA	CAC	ATT	CAG	ATT	GAT	CTT	TCT	GCA	TGG	ACC	CTC	830
2057	His	Ala	Gln	Arg	Lys	His	Ile	Gln	Ile	Asp	Leu	Ser	Ala	Trp	Thr	Leu	
2058	155					160				165						170	
2059																	
2060	AAA	TTC	AGC	AGA	AAC	CAA	AGT	CAA	CTC	CTT	GGC	CAT	CTG	TCA	GTG	GAT	878
2061	Lys	Phe	Ser	Arg	Asn	Gln	Ser	Gln	Leu	Leu	Gly	His	Leu	Ser	Val	Asp	
2062					175					180					185		
2063																	
2064	ATG	GCC	AAA	TCT	CAT	CGA	GAT	ATT	ATG	TCC	TGG	CTG	TCT	AAA	GAT	ATC	926
2065	Met	Ala	Lys	Ser	His	Arg	Asp	Ile	Met	Ser	Trp	Leu	Ser	Lys	Asp	Ile	
2066				190					195					200			
2067																	
2068	ACT	CAA	TTC	TTG	AGG	AAG	GCC	AAA	GAA	AAT	GAA	GAG	TTC	CTC	ATA	GGA	974
2069	Thr	Gln	Phe	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Glu	Glu	Phe	Leu	Ile	Gly	
2070			205					210					215				
2071																	
2072	TTT	AAC	ATT	ACG	TCC	AAG	GGA	CGC	CAG	CTG	CCA	AAG	AGG	AGG	TTA	CCT	1022
2073	Phe	Asn	Ile	Thr	Ser	Lys	Gly	Arg	Gln	Leu	Pro	Lys	Arg	Arg	Leu	Pro	
2074		220					225					230					
2075																	
2076	TTT	CCA	GAG	CCT	TAT	ATC	TTG	GTA	TAT	GCC	AAT	GAT	GCC	GCC	ATT	TCT	1070
2077	Phe	Pro	Glu	Pro	Tyr	Ile	Leu	Val	Tyr	Ala	Asn	Asp	Ala	Ala	Ile	Ser	
2078	235					240					245					250	
2079																	
2080	GAG	CCA	GAA	AGT	GTG	GTA	TCA	AGC	TTA	CAG	GGA	CAC	CGG	AAT	TTT	CCC	1118

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2081 Glu Pro Glu Ser Val Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro
2082 255 260 265
2083
2084 ACT GGA ACT GTT CCC AAA TGGGATAGCC ACATCAGAGC TGCCCTTTCC 1166
2085 Thr Gly Thr Val Pro Lys
2086 270
2087
2088 ATTGAGCGGA GGAAGAAGCG CTCTACTGGG GTCTTGCTGC CTCTGCAGAA CAACGAGCTT 1226
2089
2090 CCTGGGGCAG AATACCAGTA TAAAAAGGAT GAGGTGTGGG AGGAGAGAAA GCCTTACAAG 1286
2091
2092 ACCCTTCAGG CTCAGGCCCC TGAAAAGAGT AAGAATAAAA AGAAACAGAG AAAGGGGCCT 1346
2093
2094 CATCGGAAGA GCCAGACGCT CCAATTTGAT GAGCAGACCC TGAAAAAGGC AAGGAGAAAAG 1406
2095
2096 CAGTGGATTG AACCTCGGAA TTGCGCCAGG AGATACCTCA AGGTAGACTT TGCAGATATT 1466
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2098 GGCTGGAGTG AATGGATTAT CTCCCCCAAG TCCTTTGATG CCTATTATTG CTCTGGAGCA 1526
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2100 TGCCAGTTCC CCATGCCAAA GTCTTTGAAG CCATCAAATC ATGCTACCAT CCAGAGTATA 1586
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2102 GTGAGAGCTG TGGGGGTCGT TCCTGGGATT CCTGAGCCTT GCTGTGTACC AGAAAAGATG 1646
2103
2104 TCCTCACTCA GTATTTTATT CTTTGATGAA AATAAGAATG TAGTGCTTAA AGTATACCCT 1706
2105
2106 AACATGACAG TAGAGTCTTG CGCTTGCAGA TAACCTGGCA AAGAACTCAT TTGAATGCTT 1766
2107
2108 AATTCAATCT CTAGAGTCGA CGGAATTC 1794
2109
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2111 (2) INFORMATION FOR SEQ ID NO:32:
2112
2113 (i) SEQUENCE CHARACTERISTICS:
2114 (A) LENGTH: 272 amino acids
2115 (B) TYPE: amino acid
2116 (D) TOPOLOGY: linear
2117
2118 (ii) MOLECULE TYPE: protein
2119
2120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
2121
2122 Met Ala Gly Ala Ser Arg Leu Leu Phe Leu Trp Leu Gly Cys Phe Cys
2123 1 5 10 15
2124
2125 Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro Pro Phe Pro Glu Leu
2126 20 25 30
2127
2128 Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Gly Pro Asp Ser
2129 35 40 45
2130
2131 Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His Met Leu Arg Leu Tyr
2132 50 55 60

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2133
2134 Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu
2135 65 70 75 80
2136
2137 Gly Gly Ser Gln Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr
2138 85 90 95
2139
2140 Val Arg Ser Phe Arg Ala Ala Ala Ala Glu Thr Leu Glu Arg Lys Gly
2141 100 105 110
2142
2143 Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr Lys Ser Glu Asn Ile Leu
2144 115 120 125
2145
2146 Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn Ile Ser Leu
2147 130 135 140
2148
2149 Ser Cys Pro Val Ser Gly Gly Cys Ser His His Ala Gln Arg Lys His
2150 145 150 155 160
2151
2152 Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu Lys Phe Ser Arg Asn Gln
2153 165 170 175
2154
2155 Ser Gln Leu Leu Gly His Leu Ser Val Asp Met Ala Lys Ser His Arg
2156 180 185 190
2157
2158 Asp Ile Met Ser Trp Leu Ser Lys Asp Ile Thr Gln Phe Leu Arg Lys
2159 195 200 205
2160
2161 Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly Phe Asn Ile Thr Ser Lys
2162 210 215 220
2163
2164 Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro Glu Pro Tyr Ile
2165 225 230 235 240
2166
2167 Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val Val
2168 245 250 255
2169
2170 Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys
2171 260 265 270
2172
2173

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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2185
2186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
2187
2188 ATGTCTCATA ATCGTTCTAA AACTCCAAAA AATCAAGAAG CTCTGCGTAT GGCCAACGTG 60
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2190 GCAGAGAACA GCAGCAGCGA CCAGAGGCAG GCCTGTAAGA AGCAGGAGCT GTATGTCAGC 120
2191
2192 TTCCGAGACC TGGGCTGGCA GGACTGGATC ATCGCGCCTG AAGGCTACGC CGCCTACTAC 180
2193
2194 TGTGAGGGGG AGTGTGCCTT CCCTCTGAAC TCCTACATGA ACGCCACCAA CCACGCCATC 240
2195
2196 GTGCAGACGC TGGTCCACTT CATCAACCCG GAAACGGTGC CCAAGCCCTG CTGTGCGCCC 300
2197
2198 ACGCAGCTCA ATGCCATCTC CGTCCTCTAC TTCGATGACA GCTCCAACGT CATCCTGAAG 360
2199
2200 AAATACAGAA ACATGGTGGT CCGGGCCTGT GGCTGCCACT AGCTCCTCCG AGAATTCAGA 420
2201
2202 CCCTTTGGGG CCAAGTTTTT CTGGATCCT 449
2203
2204 (2) INFORMATION FOR SEQ ID NO:34:
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2206 (i) SEQUENCE CHARACTERISTICS:
2207 (A) LENGTH: 18 base pairs
2208 (B) TYPE: nucleic acid
2209 (C) STRANDEDNESS: single
2210 (D) TOPOLOGY: linear
2211
2212 (ii) MOLECULE TYPE: DNA
2213
2214
2215
2216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
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2218 CAAGAAGGAG ATATACAT 18
2219
2220 (2) INFORMATION FOR SEQ ID NO:35:
2221
2222 (i) SEQUENCE CHARACTERISTICS:
2223 (A) LENGTH: 377 base pairs
2224 (B) TYPE: nucleic acid
2225 (C) STRANDEDNESS: single
2226 (D) TOPOLOGY: linear
2227
2228 (ii) MOLECULE TYPE: DNA
2229
2230
2231
2232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
2233
2234 ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA AGTAGACTTT 60
2235
2236 GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCAAGT CCTTTGATGC CTATTATTGC 120

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2237
2238 TCTGGAGCAT GCCAGTTCCC CATGCCAAAG TCTTTGAAGC CATCAAATCA TGCTACCATC 180
2239
2240 CAGAGTATAG TGAGAGCTGT GGGGGTCGTT CCTGGGATTC CTGAGCCTTG CTGTGTACCA 240
2241
2242 GAAAAGATGT CCTCACTCAG TATTTTATTC TTTGATGAAA ATAAGAATGT AGTGCTTAAA 300
2243
2244 GTATACCCTA ACATGACAGT AGAGTCTTGC GCTTGCAGAT AACCTGGCAA AGAACTCATT 360
2245
2246 TGAATGCTTA ATTCAAT 377

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/864,692B

DATE: 06/04/93
TIME: 11:09:34
S4566

LINE ERROR

ORIGINAL TEXT

29 Wrong application Serial Number
747 Response Exceeds Line Limitations
1356 Response Exceeds Line Limitations

(A) APPLICATION NUMBER: US 07/864,692
cDNA library
#936208

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/864,692B

DATE: 06/04/93
TIME: 11:09:34
S4566

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/864,692B

DATE: 06/04/93
TIME: 11:09:34
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LINE ORIGINAL TEXT

CORRECTED TEXT